

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Goli, Surya K.

(ii) TITLE OF THE INVENTION: NOVEL TUMORIGENESIS PROTEIN

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Genomics, Inc.
(B) STREET: 3160 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/183,825
(B) FILING DATE: October 30, 1998

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/822,260
(B) FILING DATE: March 20, 1997

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0247-2 CON

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: UTRSN0T02
(B) CLONE: 2267574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Leu Ser Glu Ser Val Gln Lys Gly Phe Gln Met Leu Ala Asp
 1 5 10 15
 Pro Arg Ser Phe Asp Ser Asn Ala Phe Thr Leu Leu Leu Arg Ala Ala
 20 25 30
 Phe Gln Ser Leu Leu Asp Ala Gln Ala Asp Glu Ala Val Leu Asp His
 35 40 45
 Pro Asp Leu Lys His Ile Asp Pro Val Val Leu Lys His Cys His Ala
 50 55 60
 Ala Ala Ala Thr Tyr Ile Leu Glu Ala Gly Lys His Arg Ala Asp Lys
 65 70 75 80
 Ser Thr Leu Ser Thr Tyr Leu Glu Asp Cys Lys Phe Asp Arg Glu Arg
 85 90 95
 Ile Glu Leu Phe Cys Thr Glu Tyr Gln Asn Asn Lys Asn Ser Leu Glu
 100 105 110
 Ile Leu Leu Gly Ser Ile Gly Arg Ser Leu Pro His Ile Thr Asp Val
 115 120 125
 Ser Trp Arg Leu Glu Tyr Gln Ile Lys Thr Asn Gln Leu His Arg Met
 130 135 140
 Tyr Arg Pro Ala Tyr Leu Val Thr Leu Ser Val Gln Asn Thr Asp Ser
 145 150 155 160
 Pro Ser Tyr Pro Glu Ile Ser Phe Ser Cys Ser Met Glu Gln Leu Gln
 165 170 175
 Asp Leu Val Gly Lys Leu Lys Asp Ala Ser Lys Ser Leu Glu Arg Ala
 180 185 190
 Thr Gln Leu
 195

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSN0T02
- (B) CLONE: 2267574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGAAGTCACG GCGCGCTCAC AATGGAGCTC TCGGAGTCG TGCAGAAAGG CTTCCAGATG
 CTGGCGGATC CGACTCCAT CGCTTCACGC TTCTCCTCCG GCGGGCATTTC
 CAGAGTCTCC TGAGCCCA GGGCGGACGAG GCGCTGTAG ATCATCCAGA CTTGAAACAT
 ATCGACCCAG TGGTTTAAAC ACATTGTCAT GCAGCAGCTG CAACTTACAT ACTAGAGGCA
 60 120 180 240 300
 GGAAGACCCAC GAGCTGACAA GTCAACTCTA AGCACITATC TAGAAGACG TAAATTTGAC
 AGAGAGCGAA TAGAACTGTT TTGACCGAA TATCAGAATA ATAAGAATTC CCTAGAAATC
 360
 CTACTGGAA ATGATAGGCAG ATCTCTCCCT CATATAACCG ATGTTTCTTG GGGCTTGGAA
 420
 TATCAGATAAA AGAACAAATCA ATCTCATAGG ATGTCAGACG CTGCATATTG GTGTGACCTTA
 480
 AGTTGACAGA AACTGATTC CCCATCCCTAT CCAGAGATTAA GTTTTGTGTTG CAGCATGGAA
 540
 CAATTACAGG ACTTGGTGGG GAAACTTAAAG ATGCTCTCGA AAAGCCTGGA AAGAGCAACT
 600
 CAGTTGTAAC TTGGGGAAAGT TAACGATCGG CCGAGTGCAG GAGGAAACCC AGAAACGCT
 660
 TGCCCTTCAGC TGAACCCACCG TTGTGCGAG CTGGATGTCCT TTTTCAGTAG AAAAGAATT
 720
 751
 TCCTTTGAA TTTATACCAT TCANCAATT T

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 265569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Glu Leu Ser Glu Ser Val Gln Arg Gly Ile Gln Thr Leu Ala Asp
 1 5 10 15
 Pro Gly Ser Phe Asp Ser Asn Ala Phe Ala Leu Leu Leu Arg Ala Ala
 20 25 30
 Phe Gln Ser Leu Leu Asp Ala Arg Ala Asp Glu Ala Ala Leu Asp His
 35 40 45
 Pro Tyr Leu Lys Gln Ile Asp Pro Val Val Leu Lys His Cys His Ala
 50 55 60
 Ala Ala Ala Thr Cys Ile Leu Glu Ala Gly Lys His Gln Val Asp Lys
 65 70 75 80
 Ser Thr Leu Ser Thr Tyr Leu Glu Asp Cys Lys Phe Asp Arg Glu Arg
 85 90 95
 Ile Glu Leu Phe Cys Thr Glu Tyr Gln Asn Asn Lys Asn Ser Leu Glu
 100 105 110
 Thr Leu Leu Gly Ser Ile Gly Arg Ser Leu Pro His Ile Thr Asp Val
 115 120 125
 Ser Trp Arg Leu Glu Tyr Gln Ile Lys Thr Asn Gln Leu His Lys Met
 130 135 140
 Tyr Arg Pro Gly Tyr Leu Val Thr Leu Asn Val Glu Asn Asn Asp Ser
 145 150 155 160
 Gln Ser Tyr Pro Glu Ile Asn Phe Ser Cys Asn Met Glu Gln Leu Gln
 165 170 175
 Asp Leu Val Gly Lys Leu Lys Asp Ala Ser Lys Ser Leu Glu Arg Ala
 180 185 190
 Thr Gln Leu
 195

PROTEIN SEQUENCES